

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations; authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____
 Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY**Type of Search****Vendors and cost where applicable**Searcher: D. SchreiberNA Sequence (#) 2

STN _____

Searcher Phone #: 308-4292AA Sequence (#) 2

Dialog _____

Searcher Location: CM1 6A03Structure (#) 2

Questel/Orbit _____

Date Searcher Picked Up: 5/5

Bibliographic _____

Dr. Link _____

Date Completed: 9

Litigation _____

Lexis/Nexis _____

Searcher Prep & Review Time: 9

Fulltext _____

Sequence Systems CompuGen commercial

Clerical Prep Time: _____

Patent Family _____

WWW/Internet _____

Online Time: 21

Other _____

Other (specify) _____

RESULT 1

Q9WTS7

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ID      Q9WTS7; PRELIMINARY; PRT; 2771 AA.
AC      Q9WTS7;
DT      01-NOV-1999 (TrEMBLrel. 12, Created)
DT      01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      Ten-m4.
GN      NRG1 OR ODZ4 OR TEN-M4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/C; TISSUE=BRAIN;
RA      Oohashi T., Zhou X., Feng K., Richter B., Moergelin M., Perez M.T.,
RA      Su W., Chiquet-Ehrismann R., Rauch U., Faessler R.;
RT      "Mouse Ten-m/Odz is a new family of dimeric type II transmembrane
RT      proteins expressed in many tissues.";
RL      J. Cell Biol. 0:0-0(1999).
DR      EMBL; AB025413; BAA77399.1; -.
DR      HSSP; P16109; 1FSB.
DR      MGD; MGI:96083; Nrg1.
DR      InterPro; IPR000561; EGF-like.
DR      InterPro; IPR001258; NHL.
DR      Pfam; PF00008; EGF; 5.
DR      Pfam; PF01436; NHL; 6.
DR      SMART; SM00181; EGF; 6.
DR      SMART; SM00001; EGF_like; 1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_8.
DR      PROSITE; PS01186; EGF_2; 7.
KW      EGF-like domain; Glycoprotein.
SQ      SEQUENCE 2771 AA; 308497 MW; 1492E1EE1A0DBF0C CRC64:

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Query Match 97.4%; Score 14422; DB 11; Length 2771;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 2673; Conservative 40; Mismatches 40; Indels 18; Gaps 3;

Qy	1	MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV	60
Db	1	MDVKERKPYRSLTRRRDAERRYTSSSADSEEGKGPQKSYSSSETLKAYDQDARLAYGSRV	60
Qy	61	KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD	120
Db	61	KDMVPQEAEEFCRTGTNFTLRELGLGEMTPPHGTLYRTDIGLPHCGYSMGASSDADLEAD	120
Qy	121	TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHRRLRTPP	180
Db	121	TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPSSLQNHRPLRTPP	180
Qy	181	PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL	240
Db	181	PPLPHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGSAQEPTHAQDNWL	240
Qy	241	LNSNIPLETRNLGKQPFLGTLQDNLIEMDILGASRHDGAYSDBGHFLFKPGGTSPLFCTTS	300
Db	241	LNSNIPLETRNLGKQPFLGTLQDNLIEMDILSASRHDGAYSDBGHFLFKPGGTSPLFCTTS	300
Qy	301	PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF	360
Db	301	PGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPSKYCNWKAALSAILISATLVILLAYF	360
Qy	361	VAMHLFGLNWHLQPMEG--QMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGTT	418
Db	361	VAMHLFGLNWHLQPMEGQMQMYEITEDTASSWPVPTDVSLYPSGGTGLETPDRKGKGAAE	420
Qy	419	GKPSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIHDPVHLKFNVS LGKAALVGI	478
Db	421	GKPSSLFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIHDPVHLKFNVS LGKAALVGI	480

Qy 479 YGRKGLPPSHTQFDFVELLDGRRLLTQEARSLEGTTPRQSRGTVPSSSHETGFIQYLDSGI 538
 Db 481 YGRKGLPPSHTQFDFVELLDGRRLLTQEARSLEGPQRQSRGPVPPSSSHETGFIQYLDSGI 540

Qy 539 WHLAFYNDGKESEVVSFLTTAIESVDNCPSNCGNGDCISGTCHCFLGFLGPDGCRASCP 598
 Db 541 WHLAFYNDGKESEVVSFLTTAIESVDNCPSNCGNGDCISGTCHCFLGFLGPDGCRASCP 600

Qy 599 VLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCE 658
 Db 601 VLCSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSSHGTCTIMGTCTICNPGYKGESCE 660

Qy 659 EVDCMDPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPS 718
 Db 661 EVDCMDPTCSSRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCNC DPS 720

Qy 719 WTGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHGTCRDGKCECS 778
 Db 721 WTGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHGTCRDGKCECS 780

Qy 779 PGWNGEHTI-----EGCPGLCNGNGRCTLDLNGWHCVCQLGWRGAGCDTSMETAC 829
 Db 781 PGWNGEHTIAHYLDRVVKEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGTGCDTSMETGC 840

Qy 830 GDSKNDNGDGLVDCMDPDCCLQPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRI 889
 Db 841 GDGKNDNGDGLVDCMDPDCCLQPLCHVNPLCLGSPDPLDIIQETQAPVSQQNLNPFYDRI 900

Qy 890 KFLVGRDSTHIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTISRQDG 949
 Db 901 KFLVGRDSTHSIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTISRQDG 960

Qy 950 SFDLVTNGGISIILRFERAPFITQEHTLWLPWDRFFVMEIIMRHEENEIPSCDLSNFAR 1009
 Db 961 SFDLVTNGGISIILRFERAPFITQEHTLWLPWDRFFVMEIIMRHEENEIPSCDLSNFAR 1020

Qy 1010 PNPVVSPLTSFASSCAEKGPIVPEIQALQEEISISGCKMRLSYLSRTPGYKSVLRI 1069
 Db 1021 PNPVVSPLTSFASSCAEKGPIVPEIQALQEEIIVAGCKMRLSYLSRTPGYKSVLRI 1080

Qy 1070 LTHPTIPFNLKVMHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYNQKVFLSEAFVSV 1129
 Db 1081 LTHPTIPFNLKVMHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYNQKVFLSEAFVSV 1140

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 Db 1141 GYEYESCPDLILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQ 1200

Qy 1190 QPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFSG 1249
 Db 1201 QPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFSG 1260

Qy 1250 NVTNILEL-----SHSPAHHYYLATDPMGAVFLSDSNSRRVFKIKSTVVVKDLVKNS 1302
 Db 1261 NVTNILEMRNKDFRHSHPAHHYYLATDPMGAVFLSDTNSRRVFKIKSTVVVKDLVKNS 1320

Qy 1303 EVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII 1362
 Db 1321 EVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRV DQNGII 1380

Qy 1363 STLLGSNDLTSARPLSCDSVMDISQVHLEWPTDLAINPMDNSLYVLDNNVVLQISENHQV 1422
 Db 1381 STLLGSNDLTSARPLSCDSVMEISQVRLEWPTDLAINPMDNSLYVLDNNVVLQISENHQV 1440

Qy 1423 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVT 1482
 Db 1441 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVT 1500

Qy 1483 TSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNI 1542
 Db 1501 TSGEISLVAGAPSGCDCKNDANCDGSGDDGYAKDAKLNTPSSLAVCADGELYVADLGNI 1560

Qy	1543	RIRFIRKNKPFLNTQNMVELSSPIDQELYLFDDTTGKHLYTQSLPTGDYLYNFTYTGDGDI	1602
Db	1561	RIRFIRKNKPFLNTQNMVELSSPIDQELYLFDDTSGKHLYTQSLPTGDYLYNFTYTGDGDI	1620
Qy	1603	TLITDNGNMVNVRRDSTGMPLWLVPDQGVVWVTMGTSALKSVTTQGHELAMMTYHGN	1662
Db	1621	THITDNGNMVNVRRDSTGMPLWLVPDQGVVWVTMGTSALRSVTTQGHELAMMTYHGN	1680
Qy	1663	SGLLATKSNENGWTTTFEYDSFGRLTNVTFPTGQVSSFRSDTDSSVHVQVETSSKDDVTI	1722
Db	1681	SGLLATKSNENGWTTTFEYDSFGRLTNVTFPTGQVSSFRSDTDSSVHVQVETSSKDDVTI	1740
Qy	1723	TTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPVTGKR	1782
Db	1741	TTNLSASGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPVTGKR	1800
Qy	1783	NVTLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRK	1842
Db	1801	NVTLPIDNGLNLVEWRQKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRK	1860
Qy	1843	FTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDQAGRITSRIF	1902
Db	1861	FTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGHIAGIQRGIMSERMEYDQAGRITSRIF	1920
Qy	1903	ADGKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI	1962
Db	1921	ADGKMWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI	1980
Qy	1963	YQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETA	2022
Db	1981	YQPPEGNASVIQDFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETA	2040
Qy	2023	GMLKTINLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNDNSFRVTSMQAVI	2082
Db	2041	GMLKTIVNLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNDNSFRVTSMQAVI	2100
Qy	2083	NETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEI	2142
Db	2101	NETPLPIDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEI	2160
Qy	2143	FRSLMYWMTVQYDNMGRVVKKELKVGOPYANTTRYSEYDADGQLQTVSINDKPLWRYSYD	2202
Db	2161	FRSLMYWMTVQYDNMGRVVKKELKVGOPYANTTRYSEYDADGQLQTVSINDKPLWRYSYD	2220
Qy	2203	LNGNLHLLSPGNSARLTPLRYDIRDRITRLGDVQYKMDDEDGFLRQRGGDIFEYNSAGLLI	2262
Db	2221	LNGNLHLLSPGNSARLTPLRYDLRDRITRLGDVQYKMDDEDGFLRQRGGDVFEYNSAGLLI	2280
Qy	2263	KAYNRAGSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNPTKVTHLYNHSSEITSY	2322
Db	2281	KAYNRAGSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNPTKVTHLYNHSSEITSY	2340
Qy	2323	YDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQI	2382
Db	2341	YDLQGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQI	2400
Qy	2383	IIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKHLSSSNVMPFNLYMFKNNNPI	2442
Db	2401	IIGYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHELWKRLSSNSIVPFHLYMFKNNNPI	2460
Qy	2443	SNSQDIKCFMTDVNSWLLTFGFQLHNVI PGYKPDMDAMEPSYELIHTQMKTQEWDN SKS	2502
Db	2461	SNSQDIKCFMTDVNSWLLTFGFQLHNVI PGYKPDMDAMEPSYELVHTQMKTQEWDN SKS	2520
Qy	2503	ILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQAPKTKKFASSGSVFGKGVKFALKDGR	2562
Db	2521	ILGVQCEVQKQLKAFVTLERFDQLYGSTITSCQAPETKKFASSGSIFGKGVKFALKDGR	2580
Qy	2563	VTTDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGGR	2622

Db 2581 VTTDIISVANEDGRRIAAILNNAHYLENLHFTIDGVDTHYFVKPGPSEGLAILGLSGGR 2640

Qy 2623 RTLENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRA 2682
|||||:|:|||||:|||||:|||||

Db 2641 RTLENGVNVTVSQINTMLSGRTRRYTDIQLQYRALCLNTRYGTTVDEEKVRVLELARQRA 2700

Qy 2683 VRQAWAREQQRLREGEGLRAWTEGEKQQVLSTGRVQGYDGFFVISVEQYPELSDSANNI 2742
|||||:|:|||||:|||||:|||||

Db 2701 VRQAWAREQQRLREGEGLRAWTDGEKQQVLNTGRVQGYDGFFVTSVEQYPELSDSANNI 2760

Qy 2743 HFMQRSEMGR 2753
|||||

Db 2761 HFMQRSEMGR 2771